Sub A1

SEQUENCE PROTOCOL

<110> Degussa AG

<120> New nucleotide sequences which code for the mikE17 gene

<130> 000561 BT

<140>
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<160> 4

<170> PatentIn Ver. 2.1

<210> 1
<211> 1890
<212> DNA
<213> Corynebacterium glutamicum

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<223> mikE17 gene

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ctttgcgcag gtgacacaat tatcccaaca gttgcaccgt aggtgcctaa aaagttcccg 120

gggcggatgt ggcccgacca cgccgggcac ctggtggcgg cgggctgcgt cgaaaagcga 180

aaatcaacaa gtttgcaaca cctcagtgcc aagagtggtt aaggtgatgg tgatcacgct 240

atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290
Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu
1 5 10

cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338
Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly
15 20 25

tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386
Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu
30 35 40 45

acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434
Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala
50 55 60

acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482
Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln
65 70 75

gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530
Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln
80 85 90

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gag ctt tcg gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg    578
Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met
     95                 100                 105

gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc    626
Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile
110                 115                 120                 125

gca gtg gat aat cgc acc aac acg cct gag gaa cgc cgt ccc atc gcg    674
Ala Val Asp Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala
                130                 135                 140

gag gcc gtg agc atg ccg cac gaa gag gtc cgc gat ttc att tac gcc    722
Glu Ala Val Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala
            145                 150                 155

cgc caa aac tac ttc gat gcc ctt gac cgc cgc gcc gaa gcc atc gcc    770
Arg Gln Asn Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala
        160                 165                 170

gcg caa ctg ggc tgg cag ccg tac gat tcc cgc gcc atg gaa gat tcg    818
Ala Gln Leu Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser
    175                 180                 185

atc gcc cgc cgc ctg caa atg gat cac gat gtc acc atc acc tcc tcc    866
Ile Ala Arg Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser
190                 195                 200                 205

aaa gag gaa tcc ggc acg ctg cac cac ttc gac ccc gag acg cgt ctg    914
Lys Glu Glu Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu
                210                 215                 220

ctg aca atc cac gca cgc ctc aac ccc ggg caa cgc gcc ttc cgc atg    962
Leu Thr Ile His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met
            225                 230                 235

gcc acc gaa ctc ggc tac cta gaa gcc aac gac ctc atc gaa ggt atc    1010
Ala Thr Glu Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile
        240                 245                 250

gtt gac gac ggc atc tgg tcc acc ccc gaa gcc cgc acc cta gcc atc    1058
Val Asp Asp Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile
    255                 260                 265

cgc ggt gtg gcc tcc tac ttc gcc gcc gcc gtg atg ctg ccc tac aaa    1106
Arg Gly Val Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys
270                 275                 280                 285

atc ttc cac tcc gag gcc gaa aaa tcc ggc tac gac atc gag tac cta    1154
Ile Phe His Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu
                290                 295                 300

ggc caa ctc ttt ggc gtg ggc tat gag aca acc gcc cac cgc ttg tcc    1202
Gly Gln Leu Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser
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acc ctg cag cgc ccc aac ctg cgc ggc atc ccc ttt acc ttc gtg cgc   1250
Thr Leu Gln Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg
        320                 325                 330

gtc gac cgc gcc ggc aac atg tcc aaa cgc caa tcc gcc acc ggc ttc   1298
Val Asp Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe
    335                 340                 345

cac ttc acc cac tac ggc ggc acc tgc ccc ctg tgg aac gtg ttt gaa   1346
His Phe Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu
350                 355                 360                 365

acc ttc acc aac ccc ggc caa gtg ctc cgc caa ttc gcg caa atg ccc   1394
Thr Phe Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro
                370                 375                 380

gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa   1442
Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu
            385                 390                 395

gcc cgg ttc ggc gaa gta gac aaa atg ttc gcc atc ggc ctg ggc tgc   1490
Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys
        400                 405                 410

gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc   1538
Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu
    415                 420                 425

cag gac ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc   1586
Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys
430                 435                 440                 445

acc cgc gag aac tgc gcg cag cgc gca ttc cca tcc gtc cac ggc cgc   1634
Thr Arg Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg
                450                 455                 460

atc aac atc gac gcg cac gaa tcc act atc gcg ccg tac taagaaaagg    1683
Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
            465                 470

agcttgcttt acgacgcacc ctgcgggggt gggttttacc ttttatgaat gatcagcaat 1743

atccgcgtaa acaccatcgg tagccagaag aacatcatcc ggggcgataa tcagggacca 1803

cccgcgtcgc cctgcgctga cgtagattcg ctcctggaga attgcagact catccaaaaa 1863

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Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro
35 40 45

Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe
50 55 60

Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met
65 70 75 80

Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser
85 90 95

Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met
100 105 110

His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp
115 120 125

Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val
130 135 140

Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn
145 150 155 160

Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu
165 170 175

Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser Ile Ala Arg
180 185 190

Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu
195 200 205

Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile
210 215 220

His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu
225 230 235 240

Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile Val Asp Asp
245 250 255

Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val
260 265 270

Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His
275 280 285

Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu
290 295 300

Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln
305 310 315 320

Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg
325 330 335

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Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr
340 345 350

His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr
355 360 365

Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg
370 375 380

Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe
385 390 395 400

Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg
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His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu
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Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu
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Asp Ala His Glu Ser Thr Ile Ala Pro Tyr
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